comparing expression of T-bet in immune cells of said siad subject to a control that is not associated with aberrant immune cell activation; and

diagnosing the subject for a disorder based on a change in expression of T-bet in immune cells of the subject as compared to the control.

Please replace the paragraph beginning at page 6, lines 32-35, with the following amended paragraph:

Figure 3A shows that T-bet is preferentially preferentailly expressed in double negative thymocytes. Panel B shows that in a survey of Th clones, T-bet expression is restricted to Th1 cells. Panel C shows western blot analysis of T-bet. Panel D shows FACS analysis of T-bet expression.

Please replace the paragraph beginning at page 9, lines 12-27, with the following amended paragraph:

Computer algorithms known in the art can be used to optimally align and compare two nucleotide or amino acid sequences to define the percent identity between the two sequences. A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) Proc. Natl. Acad. Sci. USA 87:2264-68, modified as in Karlin and Altschul (1993) Proc. Natl. Acad. Sci. USA 90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul, et al. (1990) J. Mol. Biol. 215:403-10. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., (1997) Nucleic Acids Research 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See http://www.ncbi.nlm.nih.gov. For example, the nucleotide sequences of the invention were blasted using the default Blastn matrix 1-3 with gap penalties set at: existance 5 and extension 2. The amino acid sequences of the invention were blasted using the default settings: the Blosum62 matrix with gap penalties set at existance 11 and extension 1.

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